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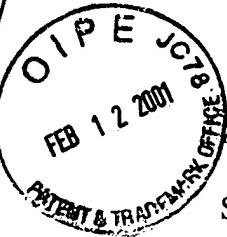
TECH CENTER 1600/2900

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TECH CENTER 1600/2900

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE



Applicant(s): Raghuram Kalluri

Serial No.: 09/543,371

Group Art Unit: 1643

Filed: April 4, 2000

Examiner: Not Assigned

For: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF
USE THEREOF

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Sir:

Although a Notice to Comply with Sequence Rules 37 C.F.R. §§1.821-1.825 has not been received in our offices, transmitted herewith is a copy of the "Sequence Listing" (sheets 1/9 through 9/9) in paper form for the above-identified patent application as required by 37 C.F.R. §1.821(c) and a copy of the "Sequence Listing" in computer readable form as required by 37 C.F.R. §1.821(e). As required by 37 C.F.R. §1.821(f), Applicant's Attorney hereby states that the content of the "Sequence Listing" in paper form and the computer readable form of the "Sequence Listing" are the same and, as required by 37 C.F.R. §1.821(g), also states that the submission includes no new matter.

Respectfully submitted,

HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

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Date: February 8, 2001



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SEQUENCE LISTING

<10> Raghuram Kalluri

<120> ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS
AND METHODS OF USE THEREOF

TECH CENTER 1600/2900

<130> 1440.1027-005

<140> US 09/543,371

<141> 2000-04-04

<150> US 09/335,224

<151> 1999-06-17

<150> US 60/089,689

<151> 1998-06-17

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<151> 1999-03-25

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48

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Asp	Pro	Gln	Cys	Pro	Ser	Gly	Thr	Lys	Ile	Leu	Tyr	His	Gly	Tyr	Ser
20															30

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35															45

144

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Thr	Ala	Gly	Ser	Cys	Leu	Arg	Lys	Phe	Ser	Thr	Met	Pro	Phe	Leu	Phe
50															

192

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Cys	Asn	Ile	Asn	Asn	Val	Cys	Asn	Phe	Ala	Ser	Arg	Asn	Asp	Tyr	Ser
65															80

240

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gcg cct gcc atg gtg atg gcc gtg cac agc cag acc att cag atc cca Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro 115 120 125	384
ccg tgc ccc agc ggg tgg tcc tcg ctg tgg atc ggc tac tct ttt gtg Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val 130 135 140	432
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<i>ff</i> cac ggc cgt ggg acc tgc aat tac tac gca aac gct tac agc ttt tgg His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp 180 185 190	576
ctc gcc acc ata gag agg agc gag atg ttc aag aag cct acg ccg tcc Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser 195 200 205	624
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35 40 45
Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
50 55 60
Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
65 70 75 80
Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile
85 90 95

Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu
 100 105 110
 Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro
 115 120 125
 Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val
 130 135 140
 Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser
 145 150 155 160
 Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
 165 170 175
 His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
 180 185 190
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48

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ctg tac ttc gag ggc cag gag aag gcg cac aac cag gac ctg ggg ctg Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu 35 40 45	144
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aac cct ggt gat gtc tgc tac tat gcc agc cgg aac gac aag tcc tac Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr 65 70 75 80	240
tgg ctc tct acc act gcg ccg ctg ccc atg atg ccc gtg gcc gag gac Trp Leu Ser Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp 85 90 95	288
gag atc aag ccc tac atc agc cgc tgt tct gtg tgt gag gcc ccg gcc Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala 100 105 110	336
<i>A</i>	
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cgc ggc acc tgc cac tac tac gcc aac aag tac agc ttc tgg ctg acc Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr 180 185 190	576
acc att ccc gag cag agc ttc cag ggc tcg ccc tcc gcc gac acg ctc Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu 195 200 205	624
aag gcc ggc ctc atc cgc aca cac atc agc cgc tgc cag gtg tgc atg Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met 210 215 220	672
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35 40 45
Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
50 55 60
Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr
65 70 75 80
Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp
85 90 95
Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala
100 105 110
Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
115 120 125
Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
130 135 140
Ala Ala Gly Asp Glu Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
145 150 155 160
Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
165 170 175
Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
180 185 190
Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
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Lys Asn Leu
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Canstatin

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Thr Thr Arg Gly Phe Val Phe Thr Arg His Ser Gln Thr Thr Ala Ile
20 25 30

cct tca tgt cca gag ggg aca gtg cca ctc tac agt ggg ttt tct ttt 144
Pro Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe
35 40 45

ctt ttt gta caa gga aat caa cga gcc cac gga caa gac ctt gga act 192
Leu Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr
50 55 60

ctt ggc agc tgc ctg cag cga ttt acc aca atg cca ttc tta ttc tgc 240
Leu Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys
65 70 75

aat gtc aat gat gta tgt aat ttt gca tct cga aat gat tat tca tac 288
Asn Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr
80 85 90 95

tgg ctg tca aca cca gct ctg atg cca atg aac atg gct ccc att act 336
Trp Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr
100 105 110

ggc aga gcc ctt gag cct tat ata agc aga tgc act gtt tgt gaa ggt 384
Gly Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly
115 120 125

cct gcg atc gcc ata gcc gtt cac agc caa acc act gac att cct cca 432
Pro Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro
130 135 140

tgt cct cac ggc tgg att tct ctc tgg aaa gga ttt tca ttc atc atg Cys Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met 145 150 155	480
ttc aca agt gca ggt tct gag ggc acc ggg caa gca ctg gcc tcc cct Phe Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro 160 165 170 175	528
ggc tcc tgc ctg gaa gaa ttc cga gcc agc cca ttt cta gaa tgt cat Gly Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His 180 185 190	576
gga aga gga acg tgc aac tac tat tca aat tcc tac agt ttc tgg ctg Gly Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu 195 200 205	624
gct tca tta aac cca gaa aga atg ttc aga aag cct att cca tca act Ala Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr 210 215 220	672
gtg aaa gct ggg gaa tta gaa aaa ata ata agt cgc tgt cag gtg tgc Val Lys Ala Gly Glu Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys 225 230 235	720
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35 40 45
Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
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37

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<223> pET22b(+) reverse oligonucleotide primer for
Tumstatin

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<212> PRT
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1 5
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Arresten

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Canstatin

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Canstatin

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